Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	433	rhodospirillum	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2005/04/19 15:37
L2	290	rhodospirillum with rubrum	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2005/04/19 15:37
L3	5	rhodospirillum with rubrum same "expression vector"	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2005/04/19 15:39
L4	91	rhodospirillum with rubrum and "expression vector"	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2005/04/19 15:39
L5	6	rhodospirillum with rubrum and "expression vector" and regulatable with promoter	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2005/04/19 15:51
L6	75	rhodospirillum with rubrum and "expression vector" and promoter	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2005/04/19 15:52
L7	62	rhodospirillum with rubrum and "expression vector" and promoter and membrane	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2005/04/19 15:52
L8	41	rhodospirillum with rubrum and "expression vector" and promoter and membrane with protein	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2005/04/19 15:52

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                   (ROSPATENT) added to list of core patent offices covered
 NEWS  4  FEB 28   PATDPAFULL - New display fields provide for legal status
                   data from INPADOC
 NEWS  5  FEB 28   BABS - Current-awareness alerts (SDIs) available
 NEWS  6  FEB 28   MEDLINE/LMEDLINE reloaded
 NEWS  7  MAR 02   GBFULL: New full-text patent database on STN
 NEWS  8  MAR 03   REGISTRY/ZREGISTRY - Sequence annotations enhanced
 NEWS  9  MAR 03   MEDLINE file segment of TOXCENTER reloaded
 NEWS  10 MAR 22   KOREAPAT now updated monthly; patent information enhanced
 NEWS  11 MAR 22   Original IDE display format returns to REGISTRY/ZREGISTRY
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=> index bioscience
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       AQUASCI, BIOBUSINESS, BIOCOMMERCE, BIOENG, BIOSIS, BIOTECHABS, BIOTECHDS,
       BIOTECHNO, CABA, CANCERLIT, CAPLUS, CEABA-VTB, CEN, CIN, CONFSCI, CROPB,
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75 FILES IN THE FILE LIST IN STNINDEX

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=> rhodospirillum (w) rubrum (p) "expression vector"
          0*  FILE ADISNEWS
          1   FILE AGRICOLA
          0*  FILE ANTE
          0*  FILE AQUALINE
          0*  FILE BIOCOMMERCE
          0*  FILE BIOENG
          8   FILE BIOSIS
          7*  FILE BIOTECHABS
          7*  FILE BIOTECHDS
          6*  FILE BIOTECHNO
          1   FILE CABA
          7   FILE CAPLUS
          0*  FILE CEABA-VTB
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          0*  FILE MEDICONF
          7   FILE MEDLINE
          0*  FILE NTIS
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          0*  FILE NUTRACEUT
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          0*  FILE PHARMAML
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          2   FILE TOXCENTER
          3   FILE USPATFULL
          0*  FILE WATER

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L1   QUE RHODOSPIRILLUM (W) RUBRUM (P) "EXPRESSION VECTOR"

=> d rank
F1          16   DGENE
F2           8   BIOSIS
F3           7   CAPLUS
F4           7   MEDLINE
F5           7*  BIOTECHABS
F6           7*  BIOTECHDS
F7           6   IFIPAT
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F8            6*  BIOTECHNO
F9            5   EMBASE
F10           4   LIFESCI
F11           4   SCISEARCH
F12           3   USPATFULL
F13           2   DISSABS
F14           2   TOXCENTER
F15           2*  ESBIOBASE
F16           2*  PASCAL
F17           1   AGRICOLA
F18           1   CABA
F19           1*  FEDRIP


=> file biosis caplus medline biotechabs
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=> rhodospirillum (w) rubrum (p) "expression vector"
L2          22 RHODOSPIRILLUM (W) RUBRUM (P) "EXPRESSION VECTOR"

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L3   ANSWER 1 OF 10  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
     DUPLICATE 1
TI   Host/vector system for expression of membrane proteins.

L3   ANSWER 2 OF 10  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
     DUPLICATE 2
TI   Role of the H protein in assembly of the photochemical reaction center and
     intracytoplasmic membrane in Rhodospirillum rubrum.

L3   ANSWER 3 OF 10  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
     DUPLICATE 3
TI   Conformational dynamics of a mobile loop in the NAD(H)-binding subunit of
     proton-translocating transhydrogenases from Rhodospirillum rubrum and
     Escherichia coli.

L3   ANSWER 4 OF 10  BIOSIS  COPYRIGHT (c) 2005 The Thomson Corporation  on STN
     DUPLICATE 4
TI   Gene expression of the B875 light-harvesting prepolypeptides from
     Rhodospirillum rubrum in Escherichia coli.

L3   ANSWER 5 OF 10  CAPLUS  COPYRIGHT 2005 ACS on STN
TI   Cloning and expression in Escherichia coli of the β subunit from
     Rhodospirillum rubrum F1-ATPase
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L3 ANSWER 6 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 5
TI CLONING AND EXPRESSION OF DRA-TG GENES FROM AZOSPIRILLUM-LIPOFERUM.

L3 ANSWER 7 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 6
TI MAPPING OF THE PUH MESSENGER RNAS FROM RHODOSPIRILLUM-RUBRUM EVIDENCE FOR TANDEM PROMOTERS.

L3 ANSWER 8 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 7
TI NONESSENTIALITY OF HISTIDINE 291 OF RHODOSPIRILLUM-RUBRUM RIBULOSE-BISPHOSPHATE CARBOXYLASE-OXYGENASE AS DETERMINED BY SITE-DIRECTED MUTAGENESIS.

L3 ANSWER 9 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 8
TI A RECONSTRUCTION OF THE GENE FOR RIBULOSE BISPHOSPHATE CARBOXYLASE FROM RHODOSPIRILLUM-RUBRUM THAT EXPRESSES THE AUTHENTIC ENZYME IN ESCHERICHIA-COLI.

L3 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2005 ACS on STN
TI Ribulose bisphosphate carboxylase manipulation in the hydrogen bacterium Alcaligenes eutrophus

=> d ab bib 1-10

L3 ANSWER 1 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 1
AB A method of expressing proteins is disclosed. In a preferable embodiment, the method comprises placing a DNA sequence encoding a protein or peptide and **expression vector** containing a regulatable promoter expressible in **Rhodospirillum rubrum** and expressing the protein within a bacterial host, wherein the host has extra capacity for membrane formation and wherein the host is a member of the genus Rhodospirillum.
AN 2004:111288 BIOSIS
DN PREV200400114849
TI Host/vector system for expression of membrane proteins.
AU Perille-Collins, Mary Lynne [Inventor, Reprint Author]; Cheng, Yongjian S. [Inventor]
CS Milwaukee, WI, USA
ASSIGNEE: WiSYS Technology Foundation, Inc., Madison, WI, USA
PI US 6680179 January 20, 2004
SO Official Gazette of the United States Patent and Trademark Office Patents, (Jan 20 2004) Vol. 1278, No. 3. http://www.uspto.gov/web/menu/patdata.html . e-file.
ISSN: 0098-1133 (ISSN print).
DT Patent
LA English
ED Entered STN: 25 Feb 2004
Last Updated on STN: 25 Feb 2004

L3 ANSWER 2 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 2
AB **Rhodospirillum rubrum** is a model for the study of membrane formation. Under conditions of oxygen limitation, this facultatively phototrophic bacterium forms an intracytoplasmic membrane that houses the photochemical apparatus. This apparatus consists of two pigment-protein complexes, the light-harvesting antenna (LH) and photochemical reaction center (RC). The proteins of the photochemical components are encoded by the puf operon (LHalpha, LHbeta, RC-L, and RC-M)

and by puhA (RC-H). R. rubrum puf interposon mutants do not form intracytoplasmic membranes and are phototrophically incompetent. The puh region was cloned, and DNA sequence determination identified open reading frames bchL and bchM and part of bchH; bchHLM encode enzymes of bacteriochlorophyll biosynthesis. A puhA/G115 interposon mutant was constructed and found to be incapable of phototrophic growth and impaired in intracytoplasmic membrane formation. Comparison of properties of the wild-type and the mutated and complemented strains suggests a model for membrane protein assembly. This model proposes that RC-H is required as a foundation protein for assembly of the RC and highly developed intracytoplasmic membrane. In complemented strains, expression of puh occurred under semiaerobic conditions, thus providing the basis for the development of an **expression vector**. The puhA gene alone was sufficient to restore phototrophic growth provided that recombination occurred.

AN 2000:179928 BIOSIS

DN PREV200000179928

TI Role of the H protein in assembly of the photochemical reaction center and intracytoplasmic membrane in Rhodospirillum rubrum.

AU Cheng, Yongjian S.; Brantner, Christine A.; Tsapin, Alexandre; Perille Collins, Mary Lynne [Reprint author]

CS Department of Biological Sciences, Great Lakes WATER Institute, University of Wisconsin-Milwaukee, Milwaukee, WI, 53201, USA

SO Journal of Bacteriology, (March, 2000) Vol. 182, No. 5, pp. 1200-1207. print.
CODEN: JOBAAY. ISSN: 0021-9193.

DT Article

LA English

ED Entered STN: 11 May 2000
Last Updated on STN: 4 Jan 2002

L3 ANSWER 3 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 3

AB Transhydrogenase catalyses the reversible transfer of reducing equivalents between NAD(H) and NADP(H) to the translocation of protons across a membrane. Uniquely in **Rhodospirillum rubrum**, the NAD(H)-binding subunit (called Th-s) exists as a separate subunit which can be reversibly dissociated from the membrane-located subunits. We have expressed the gene for R. rubrum Th-s in Escherichia coli to yield large quantities of protein. Low concentrations of either trypsin or endoproteinase Lys-C lead to cleavage of purified Th-s specifically at Lys227-Thr228 and Lys237-Glu238. Observations on the one-dimensional 1H-NMR spectra of Th-s before and after proteolysis indicate that the segment which straddles the cleavage sites forms a mobile loop protruding from the surface of the protein. Alanine dehydrogenase, which is very similar in sequence to the NAD(H)-binding subunit of transhydrogenase, lacks this segment. Limited proteolytic cleavage has little effect on some of the structural characteristics of Th-s (its dimeric nature, its ability to bind to the membrane-located subunits of transhydrogenase, and the short-wavelength fluorescence emission of a unique Trp residue) but does decrease the NADH-binding affinity, and does lower the catalytic activity of the reconstituted complex. The presence of NADH protects against trypsin or Lys-C cleavage, and leads to broadening, and in some cases, shifting, of NMR spectral signals associated with amino acid residues in the surface loop. This indicates that the loop becomes less mobile after nucleotide binding. Observation by NMR during a titration of Th-s with NAD+ provides evidence of a two-step nucleotide binding reaction. By introducing an appropriate stop codon into the gene coding for the polypeptide of E. coli transhydrogenase cloned into an **expression vector**, we have prepared the NAD(H)-binding domain equivalent to Th-s. The E. coli protein is sensitive to proteolysis by either trypsin or Lys-C in the mobile loop. Judging by the effect of NADH on its NMR spectrum and on the fluorescence of its Trp residues, the protein is capable of binding the nucleotide though it is

unable to dock with the membrane-located subunits of transhydrogenase from R. rubrum.
AN 1995:459471 BIOSIS
DN PREV199598473771
TI Conformational dynamics of a mobile loop in the NAD(H)-binding subunit of proton-translocating transhydrogenases from Rhodospirillum rubrum and Escherichia coli.
AU Diggle, Christine; Cotton, Nick P. J.; Grimley, Rachel L.; Quirk, Philip G.; Thomas, Christoper M.; Jackson, J. Baz [Reprint author]
CS Sch. Biochem., Univ. Birmingham, Edgbaston, Birmingham B15 2TT, UK
SO European Journal of Biochemistry, (1995) Vol. 232, No. 1, pp. 315-326. CODEN: EJBCAI. ISSN: 0014-2956.
DT Article
LA English
ED Entered STN: 27 Oct 1995
Last Updated on STN: 27 Oct 1995

L3 ANSWER 4 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 4
AB The gene coding for the prepolypeptides of alpha and beta, obtained as a 429 bp fragment from chromosomal DNA of **Rhodospirillum rubrum** S1 by polymerase chain reaction amplification, were cloned in tandem into the high-level **expression vector** pOTSNco12 for expression in Escherichia coli. The vector pOTSNco12 is a derivative of the pAS vector system, which contains the strong lambda-P-L promotor and is under tight control by the cI857 repressor encoded by the expression strain AR58. Induction of transcription from the lambda-P-L promotor is achieved by shifting the growth temperature from 32 to 42 degree C. Expression of the gene products was monitored by sodium dodecylsulfate polyacrylamide gel electrophoresis and western blotting. The expressed B875 light-harvesting prepolypeptides were located in the E. coli inner membrane and could not be removed by washing with high salt. The amount of expressed B875 light-harvesting prepolypeptides was estimated to be about 0.1% of the total soluble protein.
AN 1993:206745 BIOSIS
DN PREV199395107970
TI Gene expression of the B875 light-harvesting prepolypeptides from Rhodospirillum rubrum in Escherichia coli.
AU Ghosh, Robin [Reprint author]; Cornacchia, Luigi; Bachofen, Reinhard
CS Dep. Microbiol., Biocenter, Klingelbergstr. 70, CH-4056 Basel, Switzerland
SO Photochemistry and Photobiology, (1993) Vol. 57, No. 2, pp. 352-355. CODEN: PHCBAP. ISSN: 0031-8655.
DT Article
LA English
ED Entered STN: 23 Apr 1993
Last Updated on STN: 23 Apr 1993

L3 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2005 ACS on STN
AB The authors have transferred the gene for the β subunit of F0F1 ATPase of **Rhodospirillum rubrum** into an **expression vector**, and expressed the protein as a soluble fusion protein in E. coli. Pure β subunit, in significant quantities, can be simply purified from this extract Since the protein appears to be in its native conformation, it should be suitable for functional and structural studies. Further fusion protein can be obtained from the insol. fraction of the E. coli extract, but no attempts have yet been made to purify this fraction.
AN 1993:642256 CAPLUS
DN 119:242256
TI Cloning and expression in Escherichia coli of the β subunit from Rhodospirillum rubrum F1-ATPase
AU Baltscheffsky, M.; Nadanaciva, S.; Harris, D. A.
CS Dep. Biochem., Univ. Oxford, Oxford, OX1 3QU, UK
SO Res. Photosynth., Proc. Int. Congr. Photosynth., 9th (1992), Volume 3,

385-8. Editor(s): Murata, Norio. Publisher: Kluwer, Dordrecht, Neth.
CODEN: 59IZA5
DT Conference
LA English

L3 ANSWER 6 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 5
AB A genomic library of Azospirillum lipoferum was constructed with phage λ EMBL4 as vector. From this library, the genes encoding dinitrogenase reductase ADP-ribosyltransferase (DRAT), draT, and dinitrogenease reductase-activating glycohydrolase (DRAG), draG, were cloned by hybridization with the heterologous probes of **Rhodospirillum rubrum**. As in R. rubrum, draT is located between draG and nifH, the gene dinitrogenase reductase (a substrate for the DRAG/DRAT system). In the crude extract of Escherichia coli harboring the **expression vector** for this region, DRAT and DRAG enzyme activities were detected, confirming the identity of the cloned genes. Southern hybridization with genomic DNA from different Azospirillum spp., demonstrated a correlation between observable draTG hydridization and the biochemical demonstration of this covalent modification system.
AN 1990:238876 BIOSIS
DN PREV199089125829; BA89:125829
TI CLONING AND EXPRESSION OF DRA-TG GENES FROM AZOSPIRILLUM-LIPOFERUM.
AU FU H-A [Reprint author]; FITZMAURICE W P; ROBERTS G P; BURRIS R H
CS DEP BIOCHEMISTRY, UNIV WISCONSIN-MADISON, 420 HENRY MALL, MADISON, WIS 53706, USA
SO Gene (Amsterdam), (1990) Vol. 86, No. 1, pp. 95-98.
CODEN: GENED6. ISSN: 0378-1119.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 19 May 1990
Last Updated on STN: 24 Jun 1990

L3 ANSWER 7 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 6
AB The mRNA transcripts of **Rhodospirillum rubrum** gene puh, coding for the H subunit of the photoreaction center, and of genes flanking puh were analyzed by blot hybridization. Open reading frame G115, upstream of structural gene puh, is transcribed as a 2.25-kilobase mRNA. Gene puh itself is transcribed as two mRNAs of 1118 and 1032 nucleotides. Mung bean nuclease protection analysis shows that the puh transcripts have different 5' termini within open reading frame G115 and a unique rho-independent termination signal within open reading frame I2372. The lifetimes of the puh messages, as determined by an oxygen blockade of transcription, were 10 and 12 min for the large and small puh mRNAs, respectively. An **expression vector** carrying a chloramphenicol acetyltransferase gene was used to select promoters in DNA stretches upstream of the star points of each of these transcripts. Chloramphenicol resistance was expressed in Escherichia coli, using as a promoter a 179-nucleotide stretch upstream of the small mRNA startpoint but not from a 124-nucleotide stretch upstream of the large mRNA startpoint. The promoter for the small mRNA, designated Ppuh2, is thought to encompass in its -10 and -35 regions a σ70-like RNA polymerase recognition sequence. The region upstream of the large message startpoint contains a sequence similar in its -12 and -24 regions to promoter sequences recognized by the σ60 RNA polymerase holoenzyme. This is designated as promoter Ppuh1. Ppuh1 is proposed to be strictly regulated by light intensity and by oxygen tension while ppuh2 would be less sensitive to these parameters.
AN 1989:380500 BIOSIS
DN PREV198988061090; BA88:61090
TI MAPPING OF THE PUH MESSENGER RNAS FROM RHODOSPIRILLUM-RUBRUM EVIDENCE FOR

TANDEM PROMOTERS.
AU BERARD J [Reprint author]; BELANGER G; GINGRAS G
CS DEP BIOCHIM, UNIV MONTREAL, MONTREAL, QUE H3C 3J7, CAN
SO Journal of Biological Chemistry, (1989) Vol. 264, No. 18, pp. 10897-10903. CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
FS BA
LA ENGLISH
OS GENBANK-J04820
ED Entered STN: 17 Aug 1989
Last Updated on STN: 17 Aug 1989

L3 ANSWER 8 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 7
AB Chemical modification of spinach ribulosebisphosphate carboxylase/oxygenase by diethyl pyrocarbonate led to the conclusion that His-298 is an essential active-site residue(Igarashi, Y., McFadden, B. A., and ElGul, T. (1985) Biochemistry 24, 3957-3962). From the pH dependence of inactivation, the pKa of His-298 was observed to be .apprx. 6.8, and it was suggested that this histidine might be the essential base that initiates catalysis (Paech, C. (1985) Biochemistry 24, 3194-3199). To explore further the possible function of His-298, we have used site-directed mutagenesis to replace the corresponding residue of the **Rhodospirillum rubrum** carboxylase (His-291) with alanine. Assays of extracts of Escherichia coli JM107, harboring either the wild-type or mutant gene in an **expression vector**, revealed that the mutant protein is .apprx. 40% as active catalytically as the normal carboxylase. After purification to near homogeneity by immunoaffinity chromatography, the mutant protein was partially characterized with respect to subunit structure, kinetic parameters, and interaction with a transition-state analogue. The purified mutant carboxylase had a kcat of 1.5 s-1 and a kcat/Km of 1.7 · 104 M-1 s-1 in contrast to values of 3.6 s-1 and 6 · 105 M-1 s-1 for the normal enzyme. The high level of enzyme activity exhibited by the Ala-291 mutant excludes His-291 in the R. rubrum carboxylase (and by inference His-298 in the spinach carboxylase) as a catalytically essential residue.
AN 1986:400886 BIOSIS
DN PREV198682086366; BA82:86366
TI NONESSENTIALITY OF HISTIDINE 291 OF RHODOSPIRILLUM-RUBRUM RIBULOSE-BISPHOSPHATE CARBOXYLASE-OXYGENASE AS DETERMINED BY SITE-DIRECTED MUTAGENESIS.
AU NIYOGI S K [Reprint author]; FOOTE R S; MURAL R J; LARIMER F W; MITRA S; SOPER T S; MACHANOFF R; HARTMAN F C
CS PROTEIN ENGINEERING AND MOLECULAR MUTAGENESIS PROGRAM OF BIOLOGY DIV, OAK RIDGE NATIONAL LAB, OAK RIDGE, TENNESSEE 37831, USA
SO Journal of Biological Chemistry, (1986) Vol. 261, No. 22, pp. 10087-10092. CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 4 Oct 1986
Last Updated on STN: 4 Oct 1986

L3 ANSWER 9 OF 10 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
DUPLICATE 8
AB Escherichia coli plasmid pRR36, which expresses **Rhodospirillum rubrum** ribulose bisphosphate carboxylase/oxygenase (EC 4.1.1.39) as a fusion protein [Nargang et al., Mol. Gen. Genet. 193 (1984) 220-224], was used to construct a new clone of the carboxylase gene (rbc) whose expression product is the wild-type enzyme. This construction entailed removing all lacZ-coding sequences and a portion of the 5'-noncoding leader of the R. rubrum rbc gene. The highest specific activity of carboxylase was observed with an **expression vector** which juxtaposed the trp-lac (tac) hybrid promoter with the

R. rubrum ribosome binding site and the rbc structural gene. The carboxylase expressed in E. coli JM107 was purified to near homogeneity and based on subunit Mr and specific enzymic activity, the isolated protein appeared indistinguishable from authentic ribulose bisphosphate carboxylase from R. rubrum. N-terminal sequence analyses of the cloned enzyme verified that the cloned and wild-type enzymes are the same.

AN 1986:238928 BIOSIS
DN PREV198682003432; BA82:3432
TI A RECONSTRUCTION OF THE GENE FOR RIBULOSE BISPHOSPHATE CARBOXYLASE FROM RHODOSPIRILLUM-RUBRUM THAT EXPRESSES THE AUTHENTIC ENZYME IN ESCHERICHIA-COLI.
AU LARIMER F W [Reprint author]; MACHANOFF R; HARTMAN F C
CS BIOL DIV, OAK RIDGE NATL LAB, OAK RIDGE, TENN 37831, USA
SO Gene (Amsterdam), (1986) Vol. 41, No. 1, pp. 113-120.
CODEN: GENED6. ISSN: 0378-1119.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 7 Jun 1986
Last Updated on STN: 7 Jun 1986

L3 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2005 ACS on STN
AB Several recombinant plasmids were isolated which contained the ribulose diphosphate carboxylase (I) [9027-23-0] gene from a gene bank of A. eutrophus constructed in the cosmid vector pVK102. The I gene was then cloned in Pseudomonas aeruginosa. A high level of I activity was detected in P. aeruginosa exts. The pattern of transcription of I as analyzed by northern blotting suggested that the large and small subunit genes are cotranscribed. DNA sequencing showed the small subunit gene was located downstream from the large subunit gene, with an intergenic region of 47 base pairs. A transcription termination sequence and a putative promoter region were identified. The large subunit of 488 amino acid residues is colinear with the large subunit from tobacco, Chlamydomonas, Anacystis, Anabaena, and Synechococcus (54-57% homol.). However, the homol. with **Rhodospirillum rubrum** was only .apprx.27%. The I chromosomal promoter was subcloned, and **expression vectors** were constructed for expression of I genes from plants and other organisms in A. eutrophus.

AN 1986:162982 CAPLUS
DN 104:162982
TI Ribulose bisphosphate carboxylase manipulation in the hydrogen bacterium Alcaligenes eutrophus
AU Andersen, Kjell; Wilke-Douglas, Melinda; Caton, John
CS Calgene Inc., Davis, CA, 95616, USA
SO Biochemical Society Transactions (1986), 14(1), 29-31
CODEN: BCSTB5; ISSN: 0300-5127
DT Journal
LA English